

SUBJECT INDEX

A

- Åberg, Börje, 56
- Absciscic acid, 350
- Acetaldehyde, 428
- Acetosyringone, 589, 590
- Acyl hydrolase, 354
- Adams Act, 7
- African cassava mosaic gemini-virus
 - mutation, 219
 - spread protein homology, 225
 - systemic spread, 231
- Agrobacterium*
 - radiobacter*, 201, 433
 - plasmids, 192
 - rhizogenes*
 - evolutionary link to *Nicotiana*, 592-93
 - Ri plasmids, 195, 201, 385
 - root-inducing genes, 385-87
 - VirD1 protein, 595
 - VirD2, 596
 - tumefaciens*, 192
 - auxin gene homology to *P. s. pv. savastanoi* auxin gene, 196-97, 202, 592
 - resistance to *A. radiobacter*, 433
 - catabolic plasmids, 192
 - Ti plasmids, 195, 201
- Agrobacterium tumefaciens* and interkingdom genetic exchange, 583-618
- basics, 584
 - chemotaxis, 590
 - early events in T-DNA transmission, 588
 - evolution, 592-93
 - genetic maps of Ti plasmids, 584-85
 - host-pathogen binding, 590-91
 - host range, 591-92
 - oncogenes, 584-87
 - T-DNA transfer, 387-89
 - vir regulon, 589-90
- interkingdom genetic exchange
 - alternative transfer apparatus, 603
 - border endonuclease, 595
 - border endonuclease subunit functions, 595-96
 - cis-acting sequences, 593-94

- conjugation model, 597-603
- extracellular *virE* activity, 599-601
- integration products, 604-5
- key early experiments, 593
- other intermediates, 606
- overdrive-binding proteins, 594-95
- possible VirD2 activities, 596
- summary, 606-7
- T-strands, 597
- T-strand-endonuclease
 - bond, 601-3
- T-strand production, 597-98
- T-strand protection, 598-99
- preface, 583
- questions, 583
- Agrocin 84, 192, 201, 592
- Agrocinopine, 192, 591-92
- Agrocinopine permease, 592
- Agropine, 195
- Air pollutants
 - interactions with viruses, 178
- Alderman, Evangeline, 27
- Aldicarb, 453, 455-57
- Alfalfa mosaic virus
 - complementation, 218
 - movement form, 232
 - mutation, 219
 - spread proteins, 222-23, 225
 - detection and localization, 220-21
 - function, 227-28
- 1-Aminocyclopropane carboxylic acid, 355
- Amylovorin, 542
- Anthoxanthum latent blanching virus
 - biology and pathology, 99
 - diversity, 95
 - relatedness to hordeviruses, 101
 - structure, 100
- Aphanomyces euteiches*, 158
- Aphelenchus avenae*
 - stylet activity, 132
- Aphis gossypii*
 - citrus tristeza virus transmission, 300-1
- Apple mosaic virus, 172
- Arabidopsis mosaic virus, 167, 172, 174, 176
- Arachidonic acid, 360-62
- Armillaria mellea*
 - genetic variation, 475

Ascochyta

- pisi*
 - pisatin demethylation, 151
 - pisatin metabolism, 144
 - pisatin tolerance, 144
 - rabiei*
 - medicarpin detoxification, 145
 - medicarpin and maackian metabolism, 151-52
- ## Ash
- virus-like diseases, 172-73
- ## Aspergillus
- flavus*, 428
 - nidulans*, 146, 149-50, 466-67
 - gene expression, 473
 - versicolor, 428
 - Atkinson, George F., 5
 - Auxin, 584-85, 87
 - Avirulence plasmids, 198-99

B

- Bacillus*
 - subtilis*, 436
 - strain B-3, 435
 - thuringiensis*, 516
- Bacterial evolution
 - see Plasmids role in bacterial evolution
- Bacteriocins, 191-92
- Barley
 - composite cross-*R. secalis* pathosystem
 - composite crosses II and V, 87
 - natural infection of composite crosses II and V, 89-90
 - pathosystem, 88-89
 - R. secalis* pathogenic variation, 85-87
 - Erysiphe* pathosystem, 83
- Barley stripe mosaic virus
 - biology and pathology, 96-98
 - cytopathology, 96-97
 - effect on host genome, 97
 - factors influencing symptoms severity, 96
 - complementation, 218
 - expression and relationships of encoded polypeptides, 110-15
 - amino acid sequence alignment, 113

- conserved functional domains, 114
nucleotide binding motif, 112
diversity, 95
genome complexity, 101-4
genome structure and organization, 104-10
adenylate residues, 105
cap structure, 105
comparison to other tripartite viruses, 115-16
pseudoknotted structures, 106-8
RNAs common features, 104-5
RNA α structure, 108
RNA β , 109
RNA δ organization, 109-10
schematic representation, 104
3' tRNA-like terminus, 105-6
tyrosine-accepting region, 105-6
long distance spread, 230
relatedness to hordeiviruses, 101
spread protein homologies, 225
structure and chemical properties, 100
- Barley yellow dwarf luteovirus
movement in plants, 226
- Bateson, William, 21
- Bawden, F. C., 14
- Bean golden mosaic geminivirus
spread protein homology, 225
- Bean yellow mosaic virus, 171, 173
- Beet curly top geminivirus, 226
systemic spread, 231
- Beet necrotic yellow vein virus, 111, 114
movement in plant, 226
spread protein homologies, 225
- Beet western yellows luteovirus
movement in plants, 226
- Beijerinck, Martinus Willem, 50
- Bellodera utahensis*
feeding sites, 135
- Benzaldehyde, 428
- Benzoic acid, 381, 427
- Bipolaris maydis*
gene flow, 81
- Biological control of postharvest diseases, 425-41
antagonists
artificial introduction, 429-30
genetic engineering, 433
host/parasite/antagonist interactions, 430-33
interactions at wound site, 432
mode of action, 430-31
naturally occurring antagonists, 428-29
resistance to biocontrol agents, 433-34
future challenge, 438-39
introduction, 425-26
natural plant products, 427-28
rationale for antagonist selection and commercialization, 434
antagonists in controlled storage, 437-38
criteria for ideal antagonist, 434-35
isolation and screening process, 435-36
preparation and application methods, 436-37
resistance, 426-27
induced resistance, 427
- Biotechnology and Environment
Coordinating Staff, 566
- Biotechnology Science
Coordinating Committee, 565
- Birch
viruses, 171-72
- Björkman, Erik, 54
- Björnsthål, Yngve, 53
- Black locust
viruses, 173-74
- Botrytis*
cinerea, 362, 427-28
dispersal, 250
fabae, 250
Boyle, Lytton, 1-2
- Bremia lactucae*
avirulence
gene, 470
gene-dosage dependent expression, 472
genetic variation, 475-76
virulence variability, 84-85
- Brome mosaic virus, 105, 171, 229
barley stripe mosaic virus
genome organization comparison, 115-16
complementation, 218
pseudoknotted structures, 107-8
3' tRNA-like terminus secondary structure, 106
spread protein, 223
subliminal infections, 217
- C
- Calcium
wound reactions, 354
- Campbell, Andy, 5
- Cannon, O. S., 446
- Carbofuran, 453, 456
- Carnation etched ring caulimovirus
spread proteins, 222
homologies, 223
- Carnation Italian ringspot virus, 167
- Carnation mottle carmovirus, 229
movement mechanism, 233
spread protein homology, 225
- Cauliflower mosaic caulimovirus
subliminal infections, 217
transport protein, 222
detection, 221
function, 227-28
homologies, 223
- Ceratocystis*
fimbriata, 358
wound healing and resistance, 347-48
minor, 358
ulmi, 537
- Cercospora zeae-maydis*
quantitative resistance inheritance, 335
- Chapman, Royal Norton, 36
- Cherry leafroll virus, 171-72, 176
anatomical abnormalities
causes, 177
interaction with air pollutants, 178
- Chitinase, 362
- Chitwood, B. G., 43-44, 446
- Chloramphenicol, 193
- Chloride, 354
- Chlorogenic acid, 357, 362
- Chloroplasts
effect of barley stripe mosaic virus, 97
- Chorismate mutase, 357
- Christie, Jesse Roy, 41-45
beginnings, 42
introduction, 41-42
professional nematologist, 42-45
the man, 45
- Cinnamic acid 4-hydroxylase, 357
- Citrus tristeza virus, 291-316
control prospects, 308
control by cross protection, 308-9
disease history, 292-93
epidemic suppression attempt, 306-8

- reasons for failure, 307
- epidemiology
- environmental conditions
 - effect, 301
 - host plants effects, 301
 - strain effects, 300-1
 - transmitting aphids, 299-300
 - virus-vector relationships, 300
- host range of virus, 293-94
- differential host reaction, 294
- introduction, 291-92
- losses caused by virus, 305-6
- properties and diagnosis, 294-95
- coat protein, 297
 - double-stranded RNAs, 298-99
 - genome, 297-98
 - inclusion bodies, 299
 - purification, infectivity and serology, 295-97
- spread and control
- spatial spread, 305
 - surviving trees, 304
 - temporal spread, 302-5
- Cladosporium*
- cucumerinum*, 362, 364
 - hemileiae*, 525
- Clavibacter*
- michiganense* subsp. *nebraskense*
 - plasmids, 191
 - michiganense* subsp. *sepedonicum*
 - extracellular polysaccharides, 540-41, 545
 - plasmids, 191, 203
 - tritici*, 191
- Cobb, N. A., 42
- Cochliobolus heterostrophus*, 146, 474
- C male sterile cytoplasm-specific race, 497
- cytochrome P-450 gene, 468
- genetic variation, 475
- pisatin demethylation, 149
- plasmid, 475
- race T, 484-85
- host-specific toxins, 485-86
- selection coefficients, 84
- Coffee rust research, 503-31
- biology and epidemiology
- colonization, 506-7
 - dissemination, 507-8
 - environmental factors, 509-10
 - germination and penetration, 505-6
 - host factors, 508-9
 - infection process, 505-7
 - life cycle of fungus, 504
 - pathogen factors, 509
 - sporulation, 507
 - systems approach to epidemiology and management, 504-5
- conclusion, 525
- introduction, 503-4
- management
- breeding for resistance, 524-25
 - calendar schedule and modifications, 518-19
 - disease prediction models, 516-17
 - fungicide application timing, 522-23
 - fungicide efficiency, 523-24
 - natural enemies and biological control, 525
 - rainfall and fungicide application, 517-18
 - scheduling fungicide applications, 517-19
 - simple and complex forecast systems, 519-23
 - survival ratio forecast model, 519-22
- resistance, 510
- additivity of factors, 515
 - adult leaf, 514
 - basic level, 514, 516
 - biochemical and histopathological studies, 515-16
 - breeding, 524-25
 - coffee differentials, inheritance and rust races, 512-13
 - components, 511
 - evaluation, 510-11
 - induced protection, 516
 - intermediate virulence and resistance, 513
 - leaf age effect, 511
 - leaf retention, 514-15
 - light intensity effect, 511-12
 - major genes, 515
 - minor genes, 515
 - reaction type and disease intensity, 510-11
 - stabilizing selection, 513-14
 - tests, 510
 - type and durability, 514-15
 - yield effect, 512
- Colletotrichum*
- coffeanum*
 - host barrier formation, 350
 - linicola*
 - rain dispersal, 243
- Conover, Margaret Clare, 39
- Copper
- bacterial resistance, 193-94
 - fungicides for coffee rust, 523
- Corn
- Cochliobolus heterostrophus*
 - selection coefficients, 84
 - Coronatine production, 194-95
 - p-Coumarate:CoA ligase, 357
 - Cowpea chlorotic mottle virus
 - subliminal infections, 217
 - systemic spread, 230
 - Cowpea mosaic comovirus
 - movement mechanism, 233
 - mutations, 219
 - spread protein, 222-23
 - function, 228
 - systemic spread, 231
 - tubular structures between cells, 222
- Cronartium*
- quercum fs fusiforme*, 375
 - direct vs indirect selection of resistance, 381
 - direct selection of disease resistant progeny, 379
 - host resistance mechanisms, 376
 - indirect selection of resistance, 382
 - rubicola*
 - host resistance mechanisms, 376
- Crop yield
- see Ozone and crop yield
- Cucumber green mottle mosaic tobamovirus, 229
- Cucumber mosaic virus, 116
- spread proteins, 222-23
 - function, 227
- Curtobacterium*
- flaccumfaciens* pv. *aortii*, 201
 - heavy metal resistance, 194
 - flaccumfaciens* pv. *poinsettiae*
 - plasmids, 191
- Cutinase, 468-69
- Cytochrome P-450 isozymes
- pisatin detoxification, 149-51
- Cytochrome p-450 monooxygenase, 467
- Cytokinin, 584-85, 587
- biosynthesis, 196
- Cytoplasmic male sterility
- see Maize, disease susceptibility inheritance
- D
- 1,3-D, 455, 457
 - D-D Mixture, 451, 455
 - Debaryomyces hansenii*, 435
 - Dickson, J. G., 26
 - Disease susceptibility in maize
 - see Maize, disease susceptibility inheritance

- Dithiocarbamates, 523-24
Diitylenchus dipsaci, 129
 pectic enzymes, 135
 DNA
 homology, 272
 mediated transformation systems, 464
 Dodds, K. S., 21
 trans-2-Dodecenedioic acid, 355
Dothistroma pini
 host resistance breeding
 direct vs indirect selection, 380-81
 direct selection, 379
 hazard assessment, 375
- E
- Eicosapentaenoic acid, 360-62
 Elm
 viruses, 173
 Elm mosaic virus, 176
 Elm mottle virus, 173, 176
 Environment
 see Nematology, environmental aspects
Erwinia
 amylovora, 201
 amylovorin, 542
 plasmids, 191
 plasmid stability, 205
 streptomycin resistance, 193
 thiamine prototrophy, 192
 carotovora, 256
 airborne inoculum, 257
 deposition gradients, 259
 monitoring numbers, 264
 carotovora subsp. *atroseptica*
 rain dispersal, 248
 carotovora subsp. *carotovora*, 201
 bacteriocinogenicity, 191
 erythromycin resistance, 193
 chrysanthemi, 201
 herbicola, 201
 bacteriocinogenicity, 191
 pigmentation, 192-93
 thiamine prototrophy, 192
 rubrifaciens
 HR-minus mutants, 357
 stewartii, 543
 extracellular polysaccharides and disease symptoms, 541-42
 insertion sequences, 202
 pigmentation, 192-93
 plasmids, 189
 stability, 205
 thiamine prototrophy, 192
 uredovora, 201
- Erysiphe*
 graminis f. sp. *hordei*
 quantitative resistance genetics, 331-32
 graminis f. sp. *secalis*
 quantitative resistance genetics, 333
 graminis f. sp. *tritici*
 quantitative resistance genetics, 332
 Erythromycin, 193
Erysiphe graminis
 conidia, 247
 genetic structure of populations, 83
Escherichia coli, 541-42, 598-99
 T-*urf13* expression, 495-96
 Ethane, 350
 Ethyl acetate, 428
 Ethylene, 355
 Ethylenediurea
 ozone studies
 advantages and limitations, 402-3
 effect on crop yields, 400-1
 methods, 398-99
 two-treatment studies, 399-401
 Extensin, 363-64
 Extracellular polysaccharides, 539-42, 545
- F
- Federal Insecticide, Fungicide, and Rodenticide Act, 565
 Figwort mosaic caulimovirus
 spread protein homologies, 223
 Forests
 see Viruses in forests
 Fries, Nils, 53
Fulvia fulva
 avirulence gene, 469-70
 hypersensitive response elicitor, 469
 Fungal pathogenesis, molecular
 genetic approaches, 463-81
 introduction, 463-64
 perspective, 476-77
 transformation, 464-68
 DNA-mediated systems, 464
 from protein to gene, 468-70
 genome modification, 465
 plasmids, 474-75
 race cultivar specificity control, 470-74
 RFLPs use to assess genetic variation, 475-76
 transposon tagging, 474
- Fusarium*
 culmorum
 rain dispersal, 243
 graminearum, 362
 oxysporum
 genetic variation, 475
 plasmids, 474-75
 oxysporum f. sp. *cubense*
 genetic variation, 476
 oxysporum f. sp. *pisi*
 nuclear DNA variation, 476
 sambucinum, 351
 solani, 243, 257
 deposition gradients, 257
 splash dispersal, 253
 solani f. sp. *cucurbitae*
 plasmids, 474-75
 solani f. sp. *phaseoli*
 phytoalexin detoxification, 153-54
 solani f. sp. *pisi*, 145
 pisatin demethylation, 151
Fusicoccin, 543
Fusicoccum amygdali, 543
- G
- Gardner, M. W., 26, 30
 Garren, Kenneth, 1-2
 Genetically altered organisms, regulations for research, 551-81
 biotechnology regulation
 BSCC and the coordinated framework, 565-66
 guidelines and the law, 564-65
 current and future issues
 considerations for future regulation of research, 573-76
 disciplinary insularity, 569-70
 ecologists insularity, 569-70
 existing data value and experiences for risk assessment, 572-73
 liability for research covered by law, 575-76
 methods for mitigation in the environment, 571
 microorganism mitigation and microbial ecology, 570-72
 plant pathologists insularity, 570
 regulation consistency lack, 574-75
 regulation impact, 568-69
 research guidance system, 575

- guidelines in place of regulations
 - impact monitoring, 567-68
 - research outside of laboratories, 566-67
- introduction, 551-53
 - concern with recombinant DNA, 554-55
 - definitions, 552
 - importance and safety of modified organisms, 553-54
 - recombinant DNA and biomedical research, 555
- question of release, 561
 - critiques and critics of release, 564
 - plant and animal research under containment, 563
 - release of microorganisms, 562-63
 - release of plants, 561-62
- recombinant DNA guidelines development
 - decade of change, 559-60
 - early days, 555-57
 - early prohibited research, 557-58
 - environmental impact assessment of experiments, 558-59
 - guidelines extend beyond NIH and biomedical research, 560-61
 - guidelines specify containment levels for research, 558
 - Recombinant DNA Advisory Committee, 556-61
 - summary and recommendations, 576-78
- Gibberella pulicaris*
 - lubimin detoxification, 154
 - phytoalexin metabolism, 154-55
- Geotrichum candidum*
 - host resistance development, 349
- Gibberellic acid, 276
- Globodera*
 - pallida*, 69, 443
 - rostochiensis*, 69, 443
 - egg hatching, 135
 - see also Golden nematode control
- Glomerella cingulata*, 144
- β -1,3-Glucanase, 362
- Glutamate dehydrogenase gene, 474
- Glyceollin I, 358
- Golden nematode control, 443-61
 - concluding remarks, 458-59
 - control procedures research
 - crop rotation, 451
 - host range, 450
 - host resistance, 452
 - soil fumigation, 451-52
 - control program, 455-57
 - scheme, 456
 - early program decisions, 446-48
 - future directions, 457-59
 - introduction, 443
 - nature of problem, 444-45
 - nematode description, 443-44
 - management research
 - chemical management, 452-53
 - integrated management systems, 454-55
 - resistance, 453-54
 - nematode
 - discovery in USA, 446
 - origin, 445
 - quarantine, 448-49
 - research to establish regulatory procedures
 - disinfestation, 450
 - soil processing, 450
 - survey procedures, 449-50
- Good, Joe, 44
- Gregory, P. H., 242
- H**
 - Hacskaylo, Edward, 55
 - Hatch, A. B., 55
 - Helminthosporium carbonum*, 386
 - turcicum*
 - quantitative resistance genetics, 335
 - Hemileia vastatrix*
 - dispersal, 249-50
 - see also Coffee rust research
 - Heterobasidion annosum*, 357
 - Heterodera*
 - avenae*, 68
 - glycines*, 134
 - esophageal glands, 133
 - secretory granules, 127-28
 - marionii*, 129
 - schachtii*
 - dorsal gland and pathogenesis, 129-30
 - intracellular migration, 135
 - Higgins, B. B., 1-2, 5-6, 8
 - Hirst, J. M., 242
 - Hopkins, Sir Frederick, 14
 - Hordeivirus relationships and genome organization, 95-121
 - barley stripe mosaic virus
 - expression and relationships of encoded polypeptides, 110-15
 - genome complexity, 101-4
 - genome organization comparison to other tripartite viruses, 115-16
 - genome structure and organization, 104-10
 - biology and pathology
 - anthoxanthum latent blanching virus, 99
 - barley stripe mosaic virus, 96-98
 - lychnis ringspot virus, 98-99
 - poa semilatifolius virus, 98
 - introduction, 95-96
 - prospectus, 116-17
 - relatedness among hordeviruses, 101
 - structure and chemical properties, 99-100
 - polypeptides and RNA comparison, 101
 - Host-pathogen interactions
 - see Population biology of host-pathogen interactions
 - Host range and pathogenicity genes, 199-200
 - Host-specific toxins
 - maize pathogens, 485-86
 - Hull, R., 21
 - Hydroxyacetosyringone, 589
 - 6a-Hydroxymaackain, 145
 - 3-Hydroxy-3-methylglutaryl coenzyme A reductase, 358-59, 362
 - Hydroxyproline-rich glycoproteins, 363-64
 - Hypersensitive response, 356-57
 - fungal elicitor, 469
 - I**
 - Indole-3-acetamide hydrolase, 585
 - Indoleacetic acid, 350
 - gene homology, 196-97
 - synthesis by *P. s. pv. savastanoi*, 196
 - Isoflavone reductase, 156-57
 - Isolubimin, 154
 - Isoprene metabolism in wounds, 357-59
 - outline, 359
 - J**
 - Jenkins, Wilbert, 1-2

K

- Keilin, D., 15, 19
 Kievitone
 metabolism, 153-54
 Kievitone hydratase, 153
 Klug, A., 20
 Kluyver, A. J., 56
 Kögl, Fritz, 53
 Krupa, Sagar, 55
 Kyriakopoulou, P. E., 30

L

- Leach, Julian Gilbert, 35-40
 another classic contribution
 physiologic races, parasitism, and host resistance, 36-37
 insects and plant diseases
 classic research, 35-36
 insect transmission of plant diseases book, 36
 introduction, 35
 leadership, 38-39
 personal, 39
 teaching, 37-38
 Lettuce
 Bremia lactucae population variability, 84-85
 Light
 Hemileia resistance, 511-12
 Lignin, 349-50, 355
 disease resistance, 362-63
 quantitation, 363
 Lihnell, Daniel, 54
 Lohammar, Gunnar, 56
 Lubimin, 358
 metabolism, 154-55
 Lychnis ringspot virus
 biology and pathology, 98-99
 diversity, 95
 relatedness to hordeiviruses, 101
 structure and chemical properties, 100
 M
 Maackia, 145, 150
 biosynthetic pathway, 156-57
 metabolism, 151-53
Magnaporthe grisea
 avirulence genes, 470-71
 cloning strategy, 471
 Mains, N., 26
 Maize, disease susceptibility inheritance, 482-502
 cytoplasmic male sterility and T cytoplasm maize, 486-87
 discussion and observations, 496-98
 C male sterile cytoplasm-specific race, 497
 introduction, 483-84
 gene for toxin sensitivity, 484
 host-specific toxins, 485-86
 mitochondrial genome, 488-89
 pathogens and diseases, 484-85
 tissue culture mutants, 487-88
 T-urf13 characteristics
 expression in heterologous systems, 494-96
 progenitor regions, 490
 schematic representation of the *orf221* region, 490
 sequence comparison, 492
 structure, 489-94
 translation, 494
 transcription, 493
 Maize chlorotic mottle virus
 Maize dwarf mosaic potyvirus, 229
 spread protein homology, 225
 Maize streak geminivirus
 systemic spread, 231
 Markham, A. C. C., 13
 Markham, Roy, 13-22
 administration, 20-22
 early life and education, 13-14
 introduction, 13
 other plant viruses, 19-20
 PhD research, 14-16
 ribonucleic acids, 18-19
 turnip yellow mosaic virus, 16-18
 Medicarpin, 145, 156
 metabolism, 151-53
Melampsora lini
 mutation rates, 79
 Melin, Elias, 49-57
 ancestry, 49
 doctoral thesis, 50
 early life, 49
 mycorrhizae research, 50-51
 inhibition, 55
 isotope tracer techniques, 55
 root exudates, 55
 stimulation, 55
 other groups, 56
 professorship
 appointment, 52
 goals, 52
 refugees, 54
 students, 53-54
 visiting scientists, 55
 Melin, Hilda, 49
 Melin, Samuel, 49
Meloidogyne arenaria, 134
 stylet secretions analysis, 131
incognita, 69
 cytochemical analyses of granules, 131
 esophageal glands, 125
 secretory granules, 127, 129, 132, 134
 stylet secretions analysis, 131
 subcellular granules, 134
janavica, 134
 egg hatching, 135
 esophageal glands, 125
 secretory granules, 127-28, 131-32
 Miehle, Hugo, 50
 Miquel, P., 242
 Mikola, Peitsa, 55
 Mirabilis mosaic caulimovirus
 spread protein homology, 223
 Modess, Oskar, 54
Monilinia fructicola, 428
 pisatin sensitivity, 144
 Mullen, Margaret, 15, 17, 19
Mycosphaerella pinodes, 145
 pisatin demethylation, 151
zeae-maydis
 host-specific toxins, 485
 maize pathogen, 484-85
 N
 National Biological Impact Assessment Program, 567-58, 576-77
 Naumann, Einar, 56
Nectria
 galligena, 427
 haematococca, 146, 154-56, 158-59
 cutinase, 468-69
 medicarpin and maackia metabolism, 151-53
 pisatin degradation, 148-49
 pisatin degradation and cytochrome P-450 isozymes, 149-50
 pisatin degradation and pathogenicity requirement, 153
 pisatin demethylase gene, 467
 Nematode disease-inducing secretions, 123-41
 esophageal glands
 illustration, 126
 morphology, 124-27
 secretory granules, 127-28

- feeding behavior, 128-30
 phases, 128
 functions, 134
 digestion, 136-37
 egg hatching, 134-35
 feeding site induction and maintenance, 135-36
 feeding tubes, 136
 penetration and migration in tissue, 135
 future research, 137-39
 introduction, 123-24
 nature, 130-34
- Nematology, environmental aspects, 59-75
 changing attitudes, 71
 multi-partite systems, 71
 nematology in prospect, 71-72
 glasshouse or field, 68-69
 congruence between glasshouse and field experiments, 69
 cultivar-environmental interactions, 69-70
 practical advantage vs. unrealistic conditions, 70-71
 introduction, 59
 life in the soil
 above and below ground level, 62-63
 holistic approach, 63-64
 nature of environment
 ecological network, 60
 ecological network diagram, 63
 ecological networks purpose, 62
 environmental and genetic influences, 60
 factors constituting the ecological network, 60-61
 interaction, 61
 meaning of environment, 59-60
 search for ill health causes, 64
 establishing associations, 64
 synoptic approach for improving plant health, 65-66
 thresholds, 66
 environment and tolerance, 68
 nematode numbers and plant growth, 67-68
 tolerance level, 66
 tolerance threshold, 66-67
 tolerance threshold and natural selection, 67
- Neurospora crassa*
 gene cloning problems, 472
 transposable element, 474
 Newton, W., 26
 Nienhaus, F., 29
 NIH Guidelines for Research Involving Recombinant DNA Molecules
 see Genetically altered organisms, regulations for research
- Nopaline, 195, 589, 592
- O
- Oak
 tobacco mosaic virus, 171
- Octopine, 195, 589
 Office of Recombinant DNA, 556, 559, 563
 Olive knot, 196
 Opines, 595-92
 Orton, C. R., 38
 Oxalate, 538
 Oxamyl, 453, 455-57
 Ozone and crop yield, 397-423
 concluding remarks, 417-19
 dose-response studies in open-top chambers
 field dose-response studies, 411-414
 methods, 409-11
 yield loss estimations, 412-13
 interacting factors, 414-17
 different locations, 416
 parasites and pests, 415
 partial stomatal closure, 415
 peak ozone levels, 415-16
 sulfur dioxide, 415
 introduction, 397-98
 studies with ethylenediurea
 advantages and limitations, 402
 effect in various locations, 400-1
 methods, 398-99
 two-treatment studies, 399-401
 studies with open-top field chambers
 advantages and limitations, 404-5, 408-9
 measured differences in crop yields, 406-7
 methods, 402-3
 two-treatment comparisons, 403-4
- P
- Paclobutrazol, 276
Paranectria hemileia, 525
 Pathogen inoculum
 see Rain and pathogen inoculum dispersal
- Pea
 pisatin
 cytochrome-450 isozymes, 149-51
 demethylation as essential virulence trait, 151
 detoxification as tolerance mechanism, 144-46
 induction of detoxifying enzymes, 147-49
 pathogen tolerance, 144
 Pea early browning tobravirus, 218
 spread protein, 222
 Peanuts, package approach to growing, 1-10
 decision making, 7-8
 evaluations, 8-9
 fungi, 9-10
 grants and Adams, 607
 introduction, 1
 disease control and crop production, 2
 integration of various aspects, 3
 Great Peanut Project, 1-2
 plant protection sciences, 2-4
 responsibility and education, 4-5
 white coats-dirty boots, 5-7
 Peanut chlorotic leaf streak caulimovirus
 spread protein homology, 223
 Pectate lyase, 357
Penicillium oxalicum, 362
 isopentenyl transferase, 585
Peronosclerospora sorghi
 host resistance, 334-35
 Periwinkle wilt organism, 272-74
 Perry, V. G., 44
 Phaseollidin, 153-54
 Phaseollin, 153-54
 Phaseollinisoflavan, 153-54
 Phenylalanine ammonia-lyase, 357, 362
 Phenol metabolism in wounds, 357-59
- Phoma*
exigua, 362
 airborne inoculum, 257
 monitoring inoculum, 264
 wound healing and resistance, 349

- exigua* pv. *foveata*
 splash dispersal, 248
pinodella, 145
 pisatin demethylation, 151
 Phony peach disease organism,
 271-72, 274, 285
 distribution, 278
 effects on host, 275-76
 pathological anatomy, 276
 transmission, 281
 Phytoalexin, 355, 358-59, 381,
 467, 516
 elicitation in soybean, 360
 Phytoalexin detoxification, 143-
 64
 conclusions, 159-61
 elicitation and detoxifica-
 tion of phytoalexins,
 160
 introduction, 143-44
 kievitone, 153
 pathogenicity requirement
 medicarpin and maackiain
 metabolism, 151-53
 kievitone metabolism, 153-
 54
 lubimin and rishtin
 metabolism, 154-55
 pisatin and pea diseases
 demethylation as essential
 virulence trait, 151
 detoxification as tolerance
 mechanism, 144-46
 inducibility, 147-49
 inheritance, 148
 pisatin demethylase
 specificity, 147
 selective tolerance of
 pathogen, 144
 strategies for disease control,
 155-58
 application, 158-59
 phytoalexin biosynthetic
 pathway alteration,
 155-57
 specific inhibitors use, 155
Phytophthora
cactorum, 251
infestans, 350, 358, 362, 382
 chlorogenic acid accumula-
 tion, 357
 genetic variation and
 recombination effects,
 84
 phytoalexin elicitation, 360-
 61
megakarya, 244
 aerosol dispersal, 248
megasperma f. sp. *glycinea*,
 158, 358
 phytoalexin elicitation,
 360
syringae, 362
 Pierce's disease of grapevine
 see *Xylella fastidiosa*
 Pigmentation
 bacterial survival, 193
 Pines
 see Resistance breeding in
 forest trees
 Pirie, N. W., 14-15
 Pisatin, 158
 biosynthetic pathway, 156-
 57
 pathogen
 demethylation as essential
 virulence trait, 151
 detoxification as tolerance
 mechanism, 144-46
 induction of detoxifying en-
 zymes, 147-49
 inheritance of tolerance,
 148
 tolerance, 144
 Pisatin demethylase, 154, 156
 gene, 467
 specificity, 147, 150
 Plasmalemma, 354
 Plasmids
 phytopathogenic fungi, 474-
 75
 Plasmids role in bacterial evolu-
 tion, 187-212
 concluding remarks, 204-6
 horizontal exchange, 204
 plasmid stability, 205
 ecological fitness
 catabolic pathway, 192
 bacteriocin production, 191-
 92
 pigmentation and thiamine
 prototrophy, 192-93
 resistance to antibiotics and
 heavy metals, 193-94
 genetic exchange
 chromosome mobilization,
 203-4
 conjugal transfer of plas-
 mids, 200-1
 transposable elements, 202-
 3
 host specificity and
 pathogenicity, 198-99
 avirulence plasmids, 198-99
 host range and pathogeni-
 city genes, 199-200
 hyperplasias, 195
 crown gall and hairy root,
 195
 homologies between hor-
 mone genes, 196-97
 olive and oleander knot,
 196
 introduction, 187-89
 shared gene pool, 188
 traits, 188
 occurrence in phytopathogenic
 bacteria
 conserved plasmids, 189,
 191
 distribution, 189
 list, 190
 symbiotic plasmids, 197-
 98
 toxin production, 194-95
 Plasmodesmata
 structure, 215
 virus movement, 214-16
 Plum leaf scald organism, 271-
 74
 Poa semilabent virus
 biology and pathology, 98
 diversity, 95
 relatedness to hordeivirus
 group, 101
 structure and chemical proper-
 ties, 100
 Popular mosaic virus, 174
 anatomical abnormalities
 caused, 177
 Population biology of host-
 pathogen interactions, 77-
 94
 barley composite cross-*R.*
secalis pathosystem
 composite crosses II and V,
 87
 natural infection of com-
 posite crosses II and
 V, 89-90
 pathogenic variation in *R.*
secalis, 85-87
 pathosystem, 88-89
 conclusions, 91
 genetic change in pathogen
 populations
 gene flow, 80-81
 genetic drift, 80
 mutation, 79-80
 pathogen variability, 78-
 79
 recombination, 80
 selection, 81-82
 host-pathogen systems
 barley-*Erysiphe graminis*,
 83
 corn-*Cochliobolus heteros-*
trophus, 84
 lettuce-*Bremia lactucae*,
 84-85
 potato-*Phytophthora in-*
festans, 84
 wheat-*Puccinia graminis*,
 82-83
 introduction, 77-78
 necessary genetic markers,
 78
Populus spp.
 viruses, 174

- Postharvest diseases
 see biological control of
 postharvest diseases
- Potassium, 354, 356
 pump, 544
- Potato
 Phytophthora infestans vari-
 ability, 84
 Potato cyst nematodes
 see Golden nematode control
 Potato leafroll luteovirus, 229
 complementation, 218
 movement in plants, 226
 Potato spindle tuber viroid, 600
 Potato virus X potexvirus
 complementation, 218
 Potato virus Y potexvirus
 complementation, 218
 Potex virus Sieg, 166-67
 Pratylenchus brachyurus, 69
 Price, W. C., 7-8
 Proteinase inhibitor inducing
 factor, 355
 Prune dwarf virus, 172
 Prunus necrotic ringspot virus,
 172, 176
 Pseudocercospora herpo-
 trichoides, 245
 dispersal, 257
 deposition gradients, 257,
 259
 rain, 243
 splash, 247-48, 253
 spores, 246-47
 available inoculum, 261
 germination inhibition, 261-
 62
 monitoring numbers, 263-
 64
 production and temperature,
 262
 Pseudomonas,
 mellea, 201
 putida, 433
 solanacearum, 201
 catabolic plasmids, 192
 extracellular polysacchar-
 ides and virulence,
 541
 host range and pathogeni-
 city genes, 199-200
 plasmids, 189
 plasmid evolution, 205
 syringae
 ice nucleation mutant, 433
 Snomax, 575
 sucrose release from cells,
 544
 syringae pv. *angulata*, 201
 syringae pv. *atropurpurea*,
 194
 syringae pv. *coronafaciens*
 plasmids, 191
 syringae pv. *glycinea*, 191,
 203
 antibiotic resistance, 193
 avirulence genes, 198-99
 coronatine production, 194
 syringae pv. *morsprunorum*,
 194
 chromosome mobilization,
 203-4
 syringae pv. *papulans*, 201
 streptomycin resistance,
 193
 syringae pv. *phaseolicola*,
 191, 201, 205
 plasmid with episomal
 properties, 202-3
 syringae pv. *savastanoi*
 auxin and cytokinin produc-
 tion, 196
 auxin gene homology to
 Agrobacterium auxin
 gene, 196-97, 592
 insertion sequences, 202
 syringae pv. *syringae*, 201
 hypersensitive reaction,
 356
 streptomycin resistance,
 193
 syringae pv. *tabaci*, 191, 201
 syringae pv. *tomato*, 191,
 201, 203
 avirulence genes, 199
 copper resistance, 193
 coronatine production, 194-
 95
 Puccinia
 arachidis
 dispersal, 249
 coronata, 246
 mutation rates, 79
 graminis
 gene flow, 81
 genetic drift, 80
 graminis f. sp. *tritici*
 quantitative resistance ge-
 netics, 330
 wheat pathosystem, 82-83
 hordei, 386
 quantitative resistance ge-
 netics, 328-29
 recondita f. sp. *tritici*, 386
 quantitative resistance ge-
 netics, 329-30
 sorgi
 host resistance inheritance,
 334
 striiformis
 quantitative resistance ge-
 netics, 330-31
 Pyrenopeziza brassicae, 246
 rain
 deposition gradients, 257
 dispersal, 249, 253, 257
 Pyricularia oryzae
 variability, 79
 Pythium ultimum, 151
- Q
- Quantitative resistance genetics,
 317-41
 conclusions and perspectives
 genetic basis, 335-36
 research needs, 337-38
 resistance breeding signifi-
 cance, 336-37
 experimental results, 328
 leaf rust of barley, 328-29
 maize diseases, 334-35
 powdery mildew of barley,
 331-32
 powdery mildew of rye,
 333
 powdery mildew of wheat,
 332
 septoria blotch of wheat,
 334
 wheat rusts, 329-31
 introduction, 317-18
 theory, 318-19
 effective factors number,
 326
 expectations of means and
 variances, 321-25
 genetic foundation, 318
 heritability and response to
 selection, 327-28
 heterosis and average de-
 gree of dominance,
 325-26
 metrical models, 319-20
 models, 319-21
 selection and theoretical
 distribution of
 genotypic values, 327
 statistical models, 320-21
- R
- Rain and pathogen inoculum
 dispersal, 241-70
 conclusions, 265-66
 Hemileia, 508-9
 inoculum dispersal in splash
 droplets, 250-51
 affecting factors, 253-56
 deposition gradients, 257-
 59
 dispersal process, 252
 droplet sizes, 256-57
 mechanisms, 251-53
 spores per droplet vs dro-
 plet size, 254
 theoretical models, 259-60
 introduction, 241-44
 pioneers, 242

- monitoring inoculum, 260
 affecting factors, 262
 dispersed inoculum, 262-65
 produced inoculum, 260-62
 pathogen inoculum characteristics, 244-47
 splash-dispersed pathogens, 244
 rain and wind dispersal, 247
 dry-dispersed pathogens, 248-50
 splash-dispersed pathogens, 247-48
 Raspberry ringspot virus, 176
 Recombinant DNA Advisory Committee
 see Genetically altered organisms, regulations for research
 Red clover mottle comovirus, 229
 spread protein, 221-22
 function, 228
 systemic spread, 231
 tubular structures between cells, 222
 Red clover necrotic mosaic dianthovirus
 spread proteins, 223
 Reensterna, John, 53
 Resistance
 see Quantitative resistance genetics; Wound healing and resistance
 Resistance breeding in forest trees, 373-95
 genetic uniformity and biological risk, 387-90
 expected gain from recurrent selection, 388
 genotype x environment interaction, 383-84
 introduction, 373-74
 objectives, 374
 problem analysis, 374-75
 hazard assessment importance, 375
 resistance mechanisms in pines, 376-77
 screening techniques, 377
 quantitative genetic approach, 377
 direct vs indirect selection, 381
 direct selection, 377-79
 indirect selection, 379-82
 management under recurrent selection strategy, 378
 quantitative inheritance, 384-87
 attributes of resistance mechanism system, 384-85
 possible resistance mechanism systems, 386
 summary and future research, 390-92
 Resveratrol, 156
 Resveratrol synthase, 156
 RFLPs
 chromosome walking, 470-72
 use to assess genetic variation of fungi, 475-76
Rhizobium
leguminosarum, 197, 201, 205
leguminosarum biovar viciae
 host specificity, 197
meliloti
 host-specificity genes, 199
 plasmids, 189
 symbiotic plasmids, 197-98
Rhizoctonia solani, 151
 plasmids, 474
Rhizopus stolonifer, 428, 437
Rhodococcus fascians, 201
 catabolic plasmids, 192
 plasmids, 191
 cadmium resistance, 194
Rhynchosporium secalis
 barley pathosystem
 composite crosses II and V, 87
 composite crosses II and V resistance nature, 88-89
 natural infection of composite crosses II and V, 89-90
 pathogenic variation, 85-87
 conidia, 247
 monitoring inoculum produced, 260-61
 conidia numbers, 261
 splash dispersal, 253, 256-57
 deposition gradients, 257-58
 spores per droplet vs droplet diameter, 254
 variability, 79
 Ri plasmids, 195, 201, 584, 587, 594
 Ribosylzeatin, 196
 Rishitin, 358-59
 metabolism, 154-55
 RNA
 barley stripe mosaic virus, 108-10, 112-14
 genome complexity, 101-4
 genome structure and organization, 104-10
 organization, 111
 citrus tristeza virus, 297-99
 hordeiviruses, 95, 100
 pseudoknotted structures, 107
 Robinia true mosaic virus, 173
 Rodhe, Wilhelm, 56
Rotylenchulus reniformis
 feeding sites, 135
 S
Saccharomyces cerevisiae, 516
Schizophyllum commune, 473
Sclerotinia
rolfsii, 2, 4, 6
sclerotiorum, 538
Septoria
nodorum
 splash dispersal, 247-48, 253, 257
 splash dispersal gradients, 259
 spore germination, 246
 spore germination inhibition, 262
tritici
 quantitative resistance genetics, 334
 Sernander, Rutger, 49
 Silica, 351-52
 Skottsberg, Carl, 52
 Slankis, Valdis, 54
 Smith, J. D., 18
 Smith, K. M., 13, 15-17, 20
 Snomax, 575
 Southern bean mosaic sobomovirus, 230
 complementation, 218
 spread protein homology, 225
 Squalene synthetase, 359, 362
 Steiner, Gotthold, 43
Stemphylium botryosum
 pisatin demethylation, 145-46
 Stenborg, Carl Wictor, 49
 Stepanov, K. M., 242
 Steroid glycoalkaloids, 358
 Strawberry latent ringspot virus, 173
 Streptomycin, 193, 350
 Suberin, 349-51
 disease resistance, 362-63
 quantitation, 363
 Succinoglycan, 590
 Sucrose, 544
 Sulfur dioxide, 415
 Svedberg, The, 53
 Svensson, Anders, 49
 T
 Taylor, A. L., 41-43
 Thames, Walter, 44
 Thiabendazole, 350
 Thorne, Gerald, 43

- Ti plasmids, 195, 201
 see also *Agrobacterium tumefaciens* and interkingdom genetic exchange
- Tobacco blackring nepovirus spread protein, 223
- Tobacco etch potyvirus spread protein, 222 homology, 225
- Tobacco mosaic virus, 105, 166, 172-73, 176 cell-to-cell spread, 216 complementation, 218, 229-31 long distance spread, 230 movement form, 232 mechanism, 232-33 mutation, 218-19 oaks, 171 pseudoknotted structures, 107 spread proteins, 222-23, 225 detection and localization, 219-20 function, 227-28 subliminal infections, 217
- Tobacco necrosis virus, 166-67, 172, 174, 176 birch, 172 woody hosts pathogenicity proof, 174
- Tobacco rattle virus, 172, 218 movement form, 232 spread protein, 222-23
- Tobacco ringspot virus, 172-73, 176
- Tobacco streak virus spread protein, 223
- Tobacco vein mottling potyvirus spread protein, 222 homology, 225
- Tomato aspermy cucumovirus spread protein, 223
- Tomato blackring virus, 167, 174, 176
- Tomato bushy stunt virus, 167
- Tomato golden mosaic geminivirus mutation, 219 spread protein homology, 225 systemic spread, 231
- Tomato mosaic virus, 166
- Tomato ringspot virus, 172-74
- Tomato spotted wilt virus, 173-74
- Toxic Substances Control Act, 565
- Toxins effects in plant wilting, 533-50 assay for toxins membrane function, 545 plant tissue culture, 545-46 wilt assay, 544-45
- definitions, 546 extracellular water potential, 534 embolisms role in vascular diseases, 536, 538-39 pit membrane pores plugging, 539-42 vessel network reconstruction in *Ulmus*, 537 wall structure between xylem vessels, 539 xylem structure and wilting, 534-36 genetic studies importance, 546-47 introduction, 534-55 membrane function, 542-43 assays, 545 nutrient availability, 543-44 summary, 547
- Toxoptera citricida* citrus tristeza virus transmission, 299-301
- Triadimefon, 524
- Trichoderma* sp., 429, 437
- Trimethoprim, 193
- Tryptophan monooxygenase, 584
- T-urf13* expression in heterologous systems, 494-96 progenitor regions, 490 schematic representation of the *orf221* region, 490 sequence comparison, 492 structure, 489-94 translation, 494 transcription, 493
- Turnip yellow mosaic virus Roy Markham's studies, 16-18 spread protein homology, 225
- Tylenchulus semipenetrans* feeding sites, 135
- U
- Uromyces appendiculatus*, 473 vignae, 352
- Ustilago maydis*, 472-75 mating-type system molecular genetic analysis, 465-67 parasitic forms, 464 pathogenicity gene, 465
- V
- Venturia inaequalis*, 246 dispersal, 249
- Verticillium hemiliae*, 505, 525
- leptobacterium*, 525
- psalliotae*, 505
- Virus movement in plants, 213-40 cell-to-cell spread amino acid sequence similarity in spread proteins, 224 complementation, 218 detection and localization of spread proteins, 219-22 host specificity, 229-30 movement protein function, 227-28 mutation, 218-19 sequence data, 222-25 subliminal infections, 216-18 viral-coded movement proteins, 217 virus-coded functions, 216 conclusions, 232-34 introduction, 213-14 plasmodesmata, 214-16 long-distance spread, 230-31 xylem transport, 231 movement forms, 231-32 non cell-to-cell movement, 226-27
- Viruses in forests, 165-86 anatomical abnormalities, 177-78 concluding remarks, 179-80 disease management, 178-79 epidemiology, 175-77 interactions of viruses, 178 air pollutants, 178 introduction, 165-66 list, 168-70 pathogenicity proof, 174-75 viruses in forest ecosystems, 166-67 ash, 172-73 birch, 171-72 black locust, 173-74 coniferous trees, 167-71 deciduous trees, 171-74 elm, 173 European beech, 171 oak, 171 *Populus* spp., 174 soil, 166
- W
- Waksman, Selman, 52
- Walker, J. C., 37
- Watson, James, 19
- Wheat ecological network, 63 *Puccinia* pathosystem, 82-83

- White clover cryptovirus
 cell-to-cell spread, 226
- White clover mosaic potyvirus
 spread protein homology, 225
- Wikén, Torsten, 56
- Wolf, F. A., 5
- Woodroof, Naomi, 1-2
- Wound healing and resistance,
 343-371
 conclusions, 364-65
 introduction, 343-44
 physiological and biochemical
 consequences, 352-53
 cell wall modification, 362-
 64
 cytosolic responses, 357-62
 hydrolases, 362
 hydroxyproline-rich gly-
 coproteins, 363-64
 injury effects on cell mem-
 branes, 353-54
 lignin and suberin, 362-63
 lignin and suberin
 quantification, 363
 modification by microbial
 elicitors, 359-62
 phenol and isoprene
 metabolism, 357-59
 summary, 353
 wound signals, 354-57
 wound-induced structural
 barriers
 natural and wound periderm
 development, 345-46
 other barriers, 351-52
 wound anatomy, 344-45
 wound periderm formation,
 346-48
 affecting factors, 348-50
 chemical modification of
 wound response, 350-
 51
- X
- Xanthomonas*
campestris pv. *campestris*,
 473-74
 resistance genes, 199
campestris pv. *citri*
 plasmids, 191
campestris pv. *corylina*, 201
campestris pv. *malvacearum*
 rain spread, 241
campestris pv. *vesicatoria*
 copper resistance, 193
 resistance genes, 199
campestris pv. *vitians*
 resistance genes, 199
Xylella fastidiosa, 271-90
 concluding remarks, 286
 ecology and epidemiology
 aggregation and virulence,
 282-83
 geographical distribution,
 278-79
 host colonization, 282-85
- host range, 279-81
 list of natural hosts, 280
 role of stress factors, 285-
 86
 systemic movement, 284
 transmission, 281-82
 introduction, 271-72
 pathogenesis mechanism, 274-
 75
 growth regulator imbalance,
 275-76
 phytotoxin, 275
 water stress, 276-78
 taxonomy, 272-74
 groups, 272
 nucleic acid homologies,
 272-73
 pathogenic types, 273-74
 pathovars, 274
 similarity to *Rickettsia*, 272
- Y
- Yarwood, Cecil Edmund, 25-31
 daily life, 27-28
 degree work, 26
 early years, 25-26
 marriage, 27
 retirement, 30
 students, 29-30
 work, 28-30
 Yarwood, Clare, 25
 Yarwood, Helma, 25

